

AMSH1	THNEFTITIVIVP-- KQSAGFDYCDMENVEELINVQDQHQ -- LITLGWILITPQTQTAFLS
AMSH2	THNEFTITIVIVP-- KQSAGFDYCDMENVEELINVQDQHQ -- LITLGWILITPQTQTAFLS
AMSH	MRNEFTITIVLIP-- KQSAGSEYCONTEREEELFLIQDQG -- LITLGWILITPQTQTAFLS
Rpn11	TVRVIDIVFAMPQS-- GTSVSVAVLDPVQAKMIDMLKQTGRPEMVVGWYHSHPGFGCNLS
Jabl	TMILIMDSTALPVEGTETRVNQAAAAYEYMAAYLENAKQVGRIENAIGWYSHPGYGCNLS
AMSH1	
AMSH2	
AMSH	
Rpn11	
Jabl	
AMSH1	SVLHHTHCSYQIMLPEAIAIVCSKHKDTG -- IFRILITNAGMLEVSACKKKGFH-- PH
AMSH2	SVLHHTHCSYQIMLPEAIAIVCSKHKDTG -- IFRILITNAGMLEVSACKKKGFH-- PH
AMSH	SVLHHTHCSYQIMLPEAIAIVCSKHKDTG -- EFKLTDIHINGLEKETSSCRQKGPH-- PH
Rpn11	GVVINTDOSPEALSKRAVAVVVDEIQSVKGKVVIDAERLINAANMMLGHEFRQITSNIGH
Jabl	GIVGSTOMLNQQHPEPVAVVIDPTRTISAG-- KVNLGAIRTYPRGYKPPDEGSEYQ
AMSH1	
AMSH2	
AMSH	
Rpn11	
Jabl	
AMSH1	TKEPLFLFSTICKHV-- LVKDIKI-- IVLDLR--
AMSH2	TKEPLFLFSTQKFLSGTISGTA-- EMEPLKIGYGPNGFPLLGISRS8SPSEQ
AMSH	SKDPPPLFCSCSHVT-- VVDRAV-- TITDLR--
Rpn11	INKPSIQALINGLNRHYSITINMRKNELEQKMLLNHKK SWMEGLTLDQDYSENCKHNE
Jabl	TIPLNKIEDFGVHECKQYYALEVSYFKSSLDRKILLELWNKYNVNTLSSSLITNADYTIG
AMSH1	
AMSH2	
AMSH	
Rpn11	
Jabl	
AMSH1	-----
AMSH2	-----
AMSH	-----
Rpn11	-----
Jabl	QVFDLSEKLEQSEQLGRGSFMLG-- LETHDRKSEUKLAKATRDSCKTIEAINGLMSQV
AMSH1	-----
AMSH2	-----
AMSH	-----
Rpn11	-----
Jabl	LDTIVVFK-----
AMSH1	-----
AMSH2	-----
AMSH	-----
Rpn11	-----
Jabl	IKDKLFLNQINIS

FIGURE 1

AMSH1	-----MFD HIDVS LSFEERVRALS KLGCNITISEDITPRR	35
AMSH2	MDQ PFTVNSLKKLAAMEDHTDVS LSFEERVRALS KLGCNITISEDITPRR	35
AMSH	-----MSD HGDVS LPFEDRVRALSQLGSAVEVNEDIPPRR	35
. * * * *; * *; * * * *; * *; * * * *; * *; * * * *;		
AMSH1	YFRSGVEMERMASVYLEEGNLENAAVLYNKJITLIVEKLPNHRDYQQCAV	85
AMSH2	YFRSGVEMERMASVYLEEGNLENAAVLYNKJITLIVEKLPNHRDYQQCAV	100
AMSH	YFRSGVIIIRMASIYSEEGNLENAAVLYNKJITLIVEKLPKHRDYKSAVI	85
*****; * * *; * *; * * *; * * *; * * *; * * *; * * *;		
AMSH1	PEKQDIMKKLKEIAFPRTDEKLNDLLKKYVNVEYQEYLQSKNKKAEILKK	135
AMSH2	PEKQDIMKKLKEIAFPFDEKLNDLLKKYVNVEYQEYLQSKNKKAEILKK	150
AMSH	PEKKDTVKKILKEIAFPKAEEIKAEKKRKYTKETEYNEKKKEAEELARN	135
***; * * * * * * *; * * *; * * *; * * *; * * *; * * *;		
AMSH1	LEHQRLIEAERKRIAQMRQQGLESEQFLFIEDQ LKKQE LARGQ MRSQQTS	185
AMSH2	LEHQRLIEAERKRIAQMRQQGLESEQFLFIEDQ LKKQE LARGQ MRSQQTS	200
AMSH	MAIQQELEKEKQRVRAQKQGLEQEQTAEEMIRQELEKERLKIVQEF	185
*; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *;		
AMSH1	G-LSEQIDGSALSCFS--THQNNSSLNVFADQPNKSDATNYASHSPFVNR	232
AMSH2	G-LSEQIDGSALSCFS--THQNNSSLNVFADQPNKSDATNYASHSPFVNR	247
AMSH	GVDPGLGGFLVPDILEKPSLDVPTLTVSSIQPSDCHTTVRPAKPPVDR	235
*; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *;		
AMSH1	ALTPAATLSAVQN LVVEGLRCVVLFEDLCHKFLQLAESNTVRGIETCGIL	282
AMSH2	ALTPAATLSAVQN LVVEGLRCVVLFEDLCHKFLQLAESNTVRGIETCGIL	297
AMSH	SLKPGALSNEESIPTIDGLRHVVVRGRLCPQFLQLASANIRGVETCGIL	285
*; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *;		
AMSH1	CGKLTHNFEITITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLITLGWID	332
AMSH2	CGKLTHNFEITITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLITLGWID	347
AMSH	CGKLMRNFEITITHVLIPIKQSAGSDYCTENEEELFLIQDQGLITLGWID	335
***; * * * * *; * * * *; * *; * * * * *; * *; *; *; *;		
AMSH1	TEPTQTAFLSSVILHHC SYQILMLPEAI AIVCS PKHHD TGIFRLINAGML	382
AMSH2	TEPTQTAFLSSVILHHC SYQILMLPEAI AIVCS PKHHD TGIFRLINAGML	397
AMSH	TEPTQTAFLSSVILHHC SYQMLPESVAIVCS PKFQE TGFFK LTDHG LE	385
*****; * * * * *; * * *; * * *; * *; *; *; *;		
AMSH1	EVSACKKKGJHPTKEPRLFSICKHV--LVKDIKIIIVLDL-----	421
AMSH2	EVSACKKKGJHPTKEPRLFSIQKJFLSGIISGTALEMPLKIGYGPNGFP	447
AMSH	EISSCRQKGJHPSKDPFLFCSCSHVT--VVDRAVTITDLR-----	424
*; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *; *;		
AMSH1	-----	
AMSH2	LLGISRSSSPSEQL	461
AMSH	-----	

FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTI SAGKVNLG
COP9_su5_Dm	VGRMEAVGWHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVGWHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIGMKVFGTVHSHPSCRPSEEDLSLFTRGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTFHSHPSFPYPSEGDLMFFSKFGGIHIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRFMSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGPVNLPSAIDLHFFSKNGLFHLLIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPVRTDVKATEPDAYVVLVSTRDPRHIELRSYRIVDGAVT
RadC_Ecoli	I K I N A S A L I L A H N H P S G C A E P S K A D K L I T E R I I K S C Q F M D L -- R V L D H I V I G R G E Y V S F A
HSHP.....S ..D

FIGURE 3

COP9_su5_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVVIDPTRTISAGKVNLG
 COP9_su5_Dm VGRMEAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
 COP9_su5_At AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVVIDPTRTVSAGKVEIG
 COP9_su5_Ce EGRKEKVVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVVIDPLRTMSAGKVDIG
 Pad1_Dm TGRPEMVVGWYHSHPGFGCWLSGVVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
 Pad1_Hs TGRPEMVVGWYHSHPGFGCWLSGVVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
 Sks1_Dd TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
 Pad1_Sc TGRDQMVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
 HSHP.....S'D

FIGURE 4